

SEQUENCE LISTING

<110> Conaris Research Institute GmbH

<120> Diagnostic Use of Polymorphisms in the Gene Coding for
the TNF Receptor II and Method for Detecting
Non-Responders to Anti-TNF-Therapy

<130> K51347/8

<140>

<141>

<160> 54

<170> PatentIn Ver. 2:1

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<220>

<223> Description of Artificial Sequence: Forward Primer

<400> 1

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21

<210> 2

<211> 19

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<223> Description of Artificial Sequence: Reverse Primer

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<220>

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agcctggaca acatggcgaa 19

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17

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<210> 23
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<210> 24
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<212> DNA
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<210> 28
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tgctgctgcc gctggtgaga cc 22

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tgccagcaaat gctcgccggg t 21

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<210> 36
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<210> 37
<211> 26
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<223> Description of Artificial Sequence: FAM Probe

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<210> 38
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<223> Description of Artificial Sequence: TET Probe

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<210> 39
<211> 20
<212> DNA
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<220>
<223> Description of Artificial Sequence: Forward Primer

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<210> 40
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<220>
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ctgggttctg gagtt 15

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<400> 41
agaggcagcgc agttgtggaa agcctc 26

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<210> 45
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<210> 48
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ggttttctgg aagccagagc t

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<210> 49
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<222> (156)

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Met Ala Pro Val Ala Val Trp Ala
-20 -15

gcg ctg gcc gtc gga ctg gag ctc tgg gct gcg gcg cac gcc ttg ccc 161
Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala Ala His Ala Leu Pro
-10 -5 -1 1

gcc cag gtg gca ttt aca ccc tac gcc ccg gag ccc ggg agc aca tgc 209
Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys
5 10 15

cgg ctc aga gaa tac tat gac cag aca gct cag atg tgc tgc agc aaa 257
Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys
20 25 30

tgc tcg ccg ggc caa cat gca aaa gtc ttc tgt acc aag acc tcg gac			305
Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp			
35	40	45	50
acc gtg tgt gac tcc tgt gag gac agc aca tac acc cag ctc tgg aac			353
Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn			
55	60	65	
tgg gtt ccc gag tgc ttg agc tgt ggc tcc cgc tgt agc tct gac cag			401
Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln			
70	75	80	
gtg gaa actcaa gcc tgc act cgg gaa cag aac cgc atc tgc acc tgc			449
Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys			
85	90	95	
agg ccc ggc tgg tac tgc gcg ctg agc aag cag gag ggg tgc cgg ctg			497
Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg Leu			
100	105	110	
tgc gcg ccg ctg cgc aag tgc cgc ccc ggc ttc ggc gtg gcc aga cca			545
Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala Arg Pro			
115	120	125	130
gga act gaa aca tca gac gtg gtg tgc aag ccc tgt gcc ccc ggg acg			593
Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr			
135	140	145	
ttc tcc aac acg act tca tcc acg gat att tgc agg ccc cac cag atc			641
Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile			
150	155	160	
tgt aac gtg gtg gcc atc cct ggg aat gca agc atg gat gca gtc tgc			689
Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala Val Cys			
165	170	175	
acg tcc acg tcc ccc acc cgg agt atg gcc cca ggg gca gta cac tta			737
Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val His Leu			
180	185	190	
ccc cag cca gtg tcc aca cga tcc caa cac acg cag cca act cca gaa			785
Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr Pro Glu			
195	200	205	210
ccc agc act gct cca agc acc tcc ttc ctg ctc cca atg ggc ccc agc			833
Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly Pro Ser			
215	220	225	

ccc cca gct gaa ggg agc act ggc gac ttc gct ctt cca gtt gga ctg			881
Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu Pro Val Gly Leu			
230	235	240	
att gtg ggt gtg aca gcc ttg ggt cta cta ata ata gga gtg gtg aac			929
Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile Gly Val Val Asn			
245	250	255	
tgt gtc atc atg acc cag gtg aaa aag aag ccc ttg tgc ctg cag aga			977
Cys Val Ile Met Thr Gln Val Lys Lys Lys Pro Leu Cys Leu Gln Arg			
260	265	270	
gaa gcc aag gtg cct cac ttg cct gcc gat aag gcc cggt aca cag			1025
Glu Ala Lys Val Pro His Leu Pro Ala Asp Lys Ala Arg Gly Thr Gln			
275	280	285	290
ggc ccc gag cag cag cac ctg ctg atc aca gcg ccg agc tcc agc agc			1073
Gly Pro Glu Gln Gln His Leu Leu Ile Thr Ala Pro Ser Ser Ser Ser			
295	300	305	
agc tcc ctg gag agc tcg gcc agt gcg ttg gac aga agg gcg ccc act			1121
Ser Ser Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg Arg Ala Pro Thr			
310	315	320	
cggt aac cag cca cag gca cca ggc gtg gag gcc agt ggg gcc ggg gag			1169
Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala Gly Glu			
325	330	335	
gcc cggt gcc agc acc ggg agc tca gat tct tcc cct ggt ggc cat ggg			1217
Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His Gly			
340	345	350	
acc cag gtc aat gtc acc tgc atc gtg aac gtc tgt agc agc tct gac			1265
Thr Gln Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser Ser Asp			
355	360	365	370
cac agc tca cag tgc tcc tcc caa gcc agc tcc aca atg gga gac aca			1313
His Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met Gly Asp Thr			
375	380	385	
gat tcc agc ccc tcg gag tcc ccg aag gac gag cag gtc ccc ttc tcc			1361
Asp Ser Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln Val Pro Phe Ser			
390	395	400	
aag gag gaa tgt gcc ttt cgg tca cag ctg gag acg cca gag acc ctg			1409
Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu Thr Pro Glu Thr Leu			
405	410	415	

ctg ggg agc acc gaa gag aag ccc ctg ccc ctt gga gtg cct gat gct 1457
Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro Asp Ala
420 425 430

ggg atg aag ccc agt taa ccaggccggt gtgggctgtg tcgttagccaa 1505
Gly Met Lys Pro Ser
435 440

ggtgtggctga gccctggcag gatgaccctg cgaaggggcc ctggtccttc caggccccca 1565

ccactaggac tctgaggctc tttctggcc aagttcctct agtgcctcc acagccgcag 1625

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agtgcgtgtgg cctggcaag ataacgcact tctaactaga aatctgccaa ttttttaaaa 2525

aagtaagtac cactcaggcc aacaagccaa cgacaaagcc aaactctgcc agccacatcc 2585

aaccccccac ctgccatttg caccctccgc cttcaactccg gtgtgcctgc agccccgcgc 2645

ctccttcctt gctgtcctag gccacaccat ctccctttag ggaatttcag gaactagaga 2705

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20 25 30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
35 40 45

Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
 50 55 60
 Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
 65 70 75 80
 Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
 85 90 95
 Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
 100 105 110
 Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
 115 120 125
 Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
 130 135 140
 Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
 145 150 155 160
 Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
 165 170 175
 Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
 180 185 190
 Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
 195 200 205
 Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
 210 215 220
 Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
 225 230 235 240
 Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
 245 250 255
 Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly
 260 265 270
 Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys
 275 280 285
 Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro
 290 295 300
 Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
 305 310 315 320
 Ile Thr Ala Pro Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser
 325 330 335
 Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly
 340 345 350
 Val Glu Ala Ser Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser
 355 360 365
 Asp Ser Ser Pro Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile
 370 375 380
 Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln
 385 390 395 400
 Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro
 405 410 415
 Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser
 420 425 430

Gln' Leu Glu Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro
435 440 445
Leu Pro Leu Gly Val Pro Asp Ala Gly Met Lys Pro Ser
450 455 460

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Met Ala Pro Val Ala Val Trp Ala
-20 -15

gcg ctg gcc gtc gga ctg gag ctc tgg gct gcg gcg cac gcc ttg ccc 161
Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala Ala His Ala Leu Pro
-10 -5 -1 1

gcc cag gtg gca ttt aca ccc tac gcc ccg gag ccc ggg agc aca tgc 209
Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys
5 10 15

cgg ctc aga gaa tac tat gac cag aca gct cag atg tgc tgc agc aag 257
Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys
20 25 30

tgc tcg ccg ggc caa cat gca aaa gtc ttc tgt acc aag acc tcg gac 305
Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp
35 40 45 50

acc gtg tgt gac tcc tgt gag gac agc aca tac acc cag ctc tgg aac 353
Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn
55 60 65

tgg gtt ccc gag tgc ttg agc tgt ggc tcc cgc tgt agc tct gac cag 401

Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln			
70	75	80	
gtg gaa actcaa gcc tgc actcg gaa cag aac cgc atc tgc acc tgc	449		
Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys			
85	90	95	
agg ccc ggc tgg tac tgc gcg ctg agc aag cag gag ggg tgc cgg ctg	497		
Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg Leu			
100	105	110	
tgc gcg ccg ctg cgc aag tgc cgc ccg ggc ttc ggc gtg gcc aga cca	545		
Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala Arg Pro			
115	120	125	130
gga act gaa aca tca gac gtg gtg tgc aag ccc tgt gcc ccg ggg acg	593		
Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr			
135	140	145	
tcc tcc aac acg act tca tcc acg gat att tgc agg ccc cac cag atc	641		
Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile			
150	155	160	
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Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala Val Cys			
165	170	175	
acg tcc acg tcc ccc acc cgg agt atg gcc cca ggg gca gta cac tta	737		
Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val His Leu			
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ccc cag cca gtg tcc aca cga tcc caa cac acg cag cca act cca gaa	785		
Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr Pro Glu			
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ccc agc act gct cca agc acc tcc ttc ctg ctc cca atg ggc ccc agc	833		
Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly Pro Ser			
215	220	225	
ccc cca gct gaa ggg agc act ggc gac ttc gct ctt cca gtt gga ctg	881		
Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu Pro Val Gly Leu			
230	235	240	
att gtg ggt gtg aca gcc ttg ggt cta cta ata ata gga gtg gtg aac	929		
Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile Gly Val Val Asn			
245	250	255	
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 Gly Pro Glu Gln Gln His Leu Leu Ile Thr Ala Pro Ser Ser Ser
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 agc tcc ctg gag agc tcg gcc agt gcg ttg gac aga agg gcg ccc act 1121
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 Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Pro Gly Gly His Gly
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 His Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met Gly Asp Thr
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 Asp Ser Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln Val Pro Phe Ser
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 Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu Thr Pro Glu Thr Leu
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 Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro Asp Ala
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Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
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Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65 70 75 80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
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Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
100 105 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
115 120 125

Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
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 Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
 145 150 155 160
 Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
 165 170 175
 Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
 180 185 190
 Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
 195 200 205
 Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
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 Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
 225 230 235 240
 Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
 245 250 255
 Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly
 260 265 270
 Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys
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 Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro
 290 295 300
 Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
 305 310 315 320
 Ile Thr Ala Pro Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser
 325 330 335
 Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly
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 Val Glu Ala Ser Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser
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 Asp Ser Ser Pro Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile
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 Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln
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 Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro
 405 410 415
 Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser
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Met Ala Pro Val Ala Val Trp Ala
-20 -15

gcg ctg gcc gga ctg gag ctc tgg gct gcg gcg cac gcc ttg ccc 161
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Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys
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Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys
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tgc tcg ccg ggc caa cat gca aaa gtc ttc tgt acc aag acc tcg gac 305
Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp
35 40 45 50

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Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn
55 60 65

tgg gtt ccc gag tgc ttg agc tgt ggc tcc cgc tgt agc tct gac cag 401
Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln
70 75 80

gtg gaa act caa gcc tgc act cgg gaa cag aac cgc atc tgc acc tgc 449
Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys
85 90 95

agg ccc ggc tgg tac tgc gcg ctg agc aag cag gag ggg tgc cgg ctg 497
Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg Leu
100 105 110

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Cys	Ala	Pro	Leu	Arg	Lys	Cys	Arg	Pro	Gly	Phe	Gly	Val	Ala	Arg	Pro	
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Gly	Thr	Glu	Thr	Ser	Asp	Val	Val	Cys	Lys	Pro	Cys	Ala	Pro	Gly	Thr	
			135						140				145			
ttc	tcc	aac	acg	act	tca	tcc	acg	gat	att	tgc	agg	ccc	cac	cag	atc	641
Phe	Ser	Asn	Thr	Thr	Ser	Ser	Thr	Asp	Ile	Cys	Arg	Pro	His	Gln	Ile	
			150						155				160			
tgt	aac	gtg	gtg	gcc	atc	cct	ggg	aat	gca	agc	agg	gat	gca	gtc	tgc	689
Cys	Asn	Val	Val	Ala	Ile	Pro	Gly	Asn	Ala	Ser	Arg	Asp	Ala	Val	Cys	
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Thr	Ser	Thr	Ser	Pro	Thr	Arg	Ser	Met	Ala	Pro	Gly	Ala	Val	His	Leu	
			180					185				190				
ccc	cag	cca	gtg	tcc	aca	cga	tcc	caa	cac	acg	cag	cca	act	cca	gaa	785
Pro	Gln	Pro	Val	Ser	Thr	Arg	Ser	Gln	His	Thr	Gln	Pro	Thr	Pro	Glu	
			195					200				205			210	
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Pro	Ser	Thr	Ala	Pro	Ser	Thr	Ser	Phe	Leu	Leu	Pro	Met	Gly	Pro	Ser	
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Pro	Pro	Ala	Glu	Gly	Ser	Thr	Gly	Asp	Phe	Ala	Leu	Pro	Val	Gly	Leu	
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att	gtg	ggt	gtg	aca	gcc	ttg	ggt	cta	cta	ata	ata	gga	gtg	gtg	aac	929
Ile	Val	Gly	Val	Thr	Ala	Leu	Gly	Leu	Leu	Ile	Ile	Gly	Val	Val	Asn	
			245						250				255			
tgt	gtc	atc	atg	acc	cag	gtg	aaa	aag	ccc	ttg	tgc	ctg	cag	aga		977
Cys	Val	Ile	Met	Thr	Gln	Val	Lys	Lys	Lys	Pro	Leu	Cys	Leu	Gln	Arg	
			260						265				270			
gaa	gcc	aag	gtg	cct	cac	ttg	cct	gcc	gat	aag	gcc	cgg	ggt	aca	cag	1025
Glu	Ala	Lys	Val	Pro	His	Leu	Pro	Ala	Asp	Lys	Ala	Arg	Gly	Thr	Gln	
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ggc	ccc	gag	cag	cag	cac	ctg	ctg	atc	aca	gct	ccg	agg	aca	agc	agc	1073
Gly	Pro	Glu	Gln	Gln	His	Leu	Leu	Ile	Thr	Ala	Pro	Ser	Ser	Ser	Ser	
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Ser Ser Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg Arg Ala Pro Thr			
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Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala Gly Glu			
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Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Pro Gly Gly His Gly			
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Thr Gln Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser Asp			
355	360	365	370
cac agc tca cag tgc tcc tcc caa gcc agc tcc aca atg gga gac aca			1313
His Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met Gly Asp Thr			
375	380	385	
gat tcc agc ccc tcg gag tcc ccg aag gac gag cag gtc ccc ttc tcc			1361
Asp Ser Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln Val Pro Phe Ser			
390	395	400	
aag gag gaa tgt gcc ttt cgg tca cag ctg gag acg cca gag acc ctg			1409
Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu Thr Pro Glu Thr Leu			
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Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro Asp Ala			
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Gly Met Lys Pro Ser			
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<213> Homo sapiens

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35 40 45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
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65 70 75 80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
85 90 95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
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Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
115 120 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
130 135 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145 150 155 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
165 170 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
180 185 190
Asn Ala Ser Arg Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
195 200 205

Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
210 215 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225 230 235 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
245 250 255
Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly
260 265 270
Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys
275 280 285
Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro
290 295 300
Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
305 310 315 320
Ile Thr Ala Pro Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser
325 330 335
Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly
340 345 350
Val Glu Ala Ser Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser
355 360 365
Asp Ser Ser Pro Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile
370 375 380
Val Asn Val Cys Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln
385 390 395 400
Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro
405 410 415
Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser
420 425 430
Gln Leu Glu Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro
435 440 445
Leu Pro Leu Gly Val Pro Asp Ala Gly Met Lys Pro Ser
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